

EXHIBIT 1

Amino acid sequence of insert of Plasmid M15pREP (pQE-Ct-Uni) #37.

MRGSHHHHHHGSACELGTPGRRVPDPTKESLSNKISLTGDTNLTNCYLDNLRYILAIL
QKTPNEGA AVTITDYL SFFDTQKEGIYFAKNLTPESGGAIGYASPN SPTVEIRD TIGPV
IFENNTCCRPFTSSNPNA AVNKIREGGAIHAONLYINHNDVVGF MKNFSYVRGGAIST
ANTFV VSENQSCFLFMDNICIQNTAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGA
IFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSDN
ITKNYGGAIYAPVVTLVDNGPTYFINNVANNKGGAIYIDGTSNSKISADRHA IIFNENI
VTNVTSANGTSTS ANPPRRNAITVASSSGEILLGAGSSQNLI FYDPIEVS NAGVSVSFN
KEADQTGSV VFSGATVNSADFHQRNLQTKTPAPLTL SNGFLCIEDHAQLTVNRFTQTGG
VVS LGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEI PLLWVEPTNNSNNY
TADTAATFSLSDVKLSLIDDYGN SPYESTDLTHALSSQPMLSISEASDNQLRSDDMDFS
GLNVPHYGWQGLWSWGWA KTQDPEPASSATITDPKKANRFHRTL LLLTWLPAGYVPSPKH
RSPLIANTLWGNMLLATESLKN SAELT PSDHPFWGITGGGLGMMVYQEPRENHPGFHMR
SSGYFAGMIAGQTH TFSLKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAK
LVGLYSYGDHNC HHFYTQGENLTSQGTFRSQTMGGAVFFDLPMKPF GSTHILTAPFLGA
LGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVL
YRQELEIATQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTF
CNYLNGEIALRF.

Nucleic acid sequence of Plasmid M15pREP (pQE-Ct-Uni) #37.

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCATGCGAGCTCGGTACCCCGGGTC
GACGGGTTCCAGATCCTACGAAAGAGTCGCTATCAAATAAAATTAGTTTGACAGGAGACAC
TCACAATCTCACTAACTGCTATCTCGATAACCTACGCTACATACTGGCTATTCTACAAAAA
CTCCCAATGAAGGAGCTGCTGTCACAATAACAGATTACCTAAGCTTTTTTGATACACAAAA
AGAAGGTATTTATTTTGCAAAAAATCTCACCCCTGAAAGTGGTGGTGCGATTGGTTATGCG
AGTCCCAATTCTCCTACCGTGAGATTTCGTGATACAATAGGTCCTGTAATCTTTGAAAATAA
TACTTGTTGCAGACCATTACATCGAGTAATCCTAATGCAGCTGTTAATAAAATAAGAGAA
GGCGGAGCCATT CATGCTCAAATCTTTACATAAATCACAATCATGATGTGGTTCGGATTTAT
GAAGAACTTTTCTTATGTCCGAGGAGGAGCCATTAGTACCGCTAATACTTTGTTGTGAGCG
AGAATCAGTCTTGTTTTCTTTTATGGACAACATCTGTATTCAAATAACAGCAGGAAAA
GGTGGCGCTATCTATGCTGGAACGAGCAATTCTTTGAGAGTAATAACTGCGATCTCTTCTT
TATCAATAACGCCTGTTGTGCAGGAGGAGCGATCTTCTCCCTATCTGTTCTCTAACAGGAA
ATCGTGGTAACATCGTTTTCTATAACAATCGCTGCTTTAAAAATGTAGAAACAGCTTCTTCA
GAAGCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGTG
GTAGGATCTTTTTTAGTGACAATATCACAAAAATTATGGCGGAGCTATTTACGCTCCTGTA

GTTACCCTAGTGGATAATGGCCCTACCTACTTTATAAACAATGTCGCCAATAATAAGGGGG
GCGCTATCTATATAGACGGAACCAGCAACTCCAAAATTTCTGCCGACCGCCATGCTATTATT
TTTAATGAAAATATTGTGACTAATGTAAGTGTGCAAATGGTACCAGTACGTCAGCTAATC
CTCCTAGAAGAAATGCAATAACAGTAGCAAGCTCCTCTGGTGAAATTCTATTAGGAGCAGG
GAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAGTTAGCAATGCAGGGGTCTCTGTGT
CCTTCAATAAGGAAGCTGATCAAACAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAATTCT
GCAGATTTTCATCAACGCAATTTACAAACAAAAACACCTGCACCCCTTACTCTCAGTAATG
GTTTTCTATGTATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAAAACCTGGGGGT
GTTGTTTCTCTTGGGAATGGAGCAGTTCTGAGTTGCTATAAAAATGGTGCAGGAAATTCTGC
TAGCAATGCCTCTATAACACTGAAGCATATTGGATTGAATCTTTCTTCCATTCTGAAAAGTG
GTGCTGAGATTCTTTATTGTGGGTAGAGCCTACAAATAACAGCAATAACTATACAGCAGA
TACTGCAGCTACCTTTTCATTAAGTGATGTAAAACCTCTCACTCATTGATGACTATGGGAATT
CTCCTTATGAATCCACAGATCTAACCCATGCTCTGTCATCACAGCCTATGCTATCTATTTCT
GAGGCTAGTGATAACCAGCTAAGATCTGATGATATGGATTTCTCGGGACTAAATGTCCCTC
ATTATGGATGGCAAGGACTTTGGAGTTGGGGCTGGGCAAAAACCTCAAGATCCAGAACCAG
CATCTTCAGCAACAATCACAGATCCCAAAAAAGCCAATAGATTCCATAGAACCTTATTACT
GACTTGGCTTCCTGCTGGGTATGTTCTAGCCCGAAACACAGAAGTCCCCTCATAGCGAAT
ACCTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAATAGTGCAGAACTGACAC
CTAGTGATCATCCTTTCTGGGGAATTACAGGAGGAGGACTAGGCATGATGGTTTACCAAGA
ACCTCGAGAAAATCATCCTGGATTCCATATGCGCTCTTCCGGATACTTTGCGGGGATGATA
GCAGGGCAAACACATACCTTCTCATTGAAATTCAGTCAGACCTACACCAAACCTCAATGAGC
GTTACGCAAAAAACAACGTATCTTCTAAAAATTACTCATGCCAAGGAGAAATGCTCTTCTC
ATTGCAAGAAGGTTTCTTGCTGGCTAAATTAGTTGGTCTTTACAGCTATGGAGATCATAACT
GTCACCATTTCTATACCCAAGGAGAAAATCTAACATCTCAAGGGACGTTCCGTAGTCAAAC
GATGGGAGGTGCTGTTTTTTTTGATCTCCCTATGAAACCCTTTGGATCAACGCATATACTGA
CAGCTCCCTTTTTAGGTGCTCTTGGTATTTATTCTAGCCTGTCTCACTTTACTGAGGTGGGAG
CCTATCCGCGAAGCTTTTCTACAAAGACTCCTTTGATCAATGTCCTAGTCCCTATTGGAGTT
AAAGGTAGCTTTATGAATGCTACCCAAAGACCTCAAGCCTGGACTGTAGAATTGGCATACC
AACCCGTTCTGTATAGACAAGAACTAGAGATCGCGACCCAGCTCCTAGCCAGTAAAGGTAT
TTGGTTTGGTAGTGGAAGCCCCTCATCGCGTCATGCCATGTCCTATAAAATCTCACAGCAAA
CACAACTTTGAGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCCTCTTCAACCT
TCTGTAATTATCTCAATGGGGAAATTGCTCTGCGATTCTAA



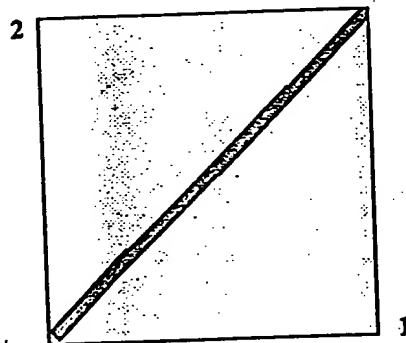
Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq_1 Length 956 (1..956)

Sequence 2 lc|seq_2 Length 965 (1..965)



NOT: (score and expect value) is calculated based on the size of nr database

Score = 1885 bits (4884), Expect = 0.0
Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK 82
VPDPTKESLSNKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK
Sbjct: 32 VPDPTKESLSNKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK 91

Query: 83 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR 142
EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR
Sbjct: 92 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR 151

Query: 143 EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQNT 202
EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQNT
Sbjct: 152 EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQNT 211

Query: 203 AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 262
AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV
Sbjct: 212 AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 271

Query: 263 ETASSEASDGGAIKVTTRLDVGTNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN 322
ETASSEASDGGAIKVTTRLDVGTNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN
Sbjct: 272 ETASSEASDGGAIKVTTRLDVGTNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN 331

Query: 323 VANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTSANGTSTSANPPRRNAITVASS 382
+ANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVT+ANGTSTSANPPRRNAITVASS
Sbjct: 332 IANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTNANGTSTSANPPRRNAITVASS 391

Query: 383 GEILLGAGSSQNLIFYPDIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK 442
GEILLGAGSSQNLIFYPDIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK
Sbjct: 392 GEILLGAGSSQNLIFYPDIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK 451

Query: 443 TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 502
TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH
Sbjct: 452 TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 511

Query: 503 IGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDL 562
IGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDL

Friday, September 6, 2001

Blast Result

Subject: 512 IGLNLSSILKSGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKLSLIDYGNSPYESTDL 571
 Query: 563 THALSSQPMLSISEASDNQLRSDDMDFSGNLVPHYGWQGLWSGWAKTQDPEPASSATIT 622
 THALSSQPMLSISEASDNQLRSDDMDFSGNLVPHYGWQGLW+GWAKTQDPEPASSATIT
 Subject: 572 THALSSQPMLSISEASDNQLRSDDMDFSGNLVPHYGWQGLWTGWAKTQDPEPASSATIT 631
 Query: 623 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP 682
 DP+KANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP
 Subject: 632 DPQKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP 691
 Query: 683 WGITGGGLGMMVYQEPRENHPGFHMRRSSGYFAGMIAGQTHTFSLKFSQTYTKLNERYAKN 742
 WGITGGGLGMMVYQ+PRENHPGFHMRRSSGY AGMIAGQTHTFSLKFSQTYTKLNERYAKN
 Subject: 692 WGITGGGLGMMVYQDPRENHPGFHMRRSSGYSAGMIAGQTHTFSLKFSQTYTKLNERYAKN 751
 Query: 743 NVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMG 802
 NVSSKNYSCQGEMLFSLQEGFLL KLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMG
 Subject: 752 NVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMG 811
 Query: 803 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 862
 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK
 Subject: 812 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 871
 Query: 863 GSFMNATQRPQAWTVELAYQPVLRYRQELEIATQLLASKGIWFGSGSPSSRHMSYKISQQ 922
 GSFMNATQRPQAWTVELAYQPVLRYRQE IATQLLASKGIWFGSGSPSSRHMSYKISQQ
 Subject: 872 GSFMNATQRPQAWTVELAYQPVLRYRQEPGIATQLLASKGIWFGSGSPSSRHMSYKISQQ 931
 Query: 923 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956
 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF
 Subject: 932 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965

CPU time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

Gapped
 Lambda K H
 0.316 0.132 0.396

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 12,524
 Number of Sequences: 0
 Number of extensions: 873
 Number of successful extensions: 15
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 956
 length of database: 239,316,239
 effective HSP length: 131
 effective length of query: 825
 effective length of database: 206,523,009
 effective search space: 170381482425
 effective search space used: 170381482425
 T: 9
 A: 40
 X1: 16 (7.3 bits)
 X2: 129 (49.7 bits)
 X3: 129 (49.7 bits)
 S1: 41 (21.6 bits)
 S2: 77 (34.3 bits)